

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 101577,775A
Source: TFWO
Date Processed by STIC: 3/15/07

ENTERED



IFWO

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/577,775A

DATE: 03/15/2007
 TIME: 10:18:27

Input Set : A:\Sequence Listing.txt
 Output Set: N:\CRF4\03152007\J577775A.raw

3 <110> APPLICANT: KIM, TAE-YOON
 4 BIO CLUE & SOLUTION CO., LT
 6 <120> TITLE OF INVENTION: EC SOD and Cell transducing EC SOD and use thereof
 8 <130> FILE REFERENCE: 1012679-000121
 10 <140> CURRENT APPLICATION NUMBER: US 10/577,775A
 12 <141> CURRENT FILING DATE: 2006-04-28
 14 <150> PRIOR APPLICATION NUMBER: PCT/KR2004/002757
 15 <151> PRIOR FILING DATE: 2004-10-29
 17 <150> PRIOR APPLICATION NUMBER: KR10-2003-0076629
 18 <151> PRIOR FILING DATE: 2003-10-31
 20 <160> NUMBER OF SEQ ID NOS: 33
 22 <170> SOFTWARE: KopatentIn 1.71
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 18
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: primer
 33 <400> SEQUENCE: 1
 34 atttggcct tcttggtc 18
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 18
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Artificial Sequence
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: primer
 46 <400> SEQUENCE: 2
 47 ttaagtggtc ttgcactc 18
 50 <210> SEQ ID NO: 3
 51 <211> LENGTH: 33
 52 <212> TYPE: DNA
 53 <213> ORGANISM: Artificial Sequence
 55 <220> FEATURE:
 56 <223> OTHER INFORMATION: primer
 59 <400> SEQUENCE: 3
 60 agtctcgaga tgttggcctt ctgtttctac ggc 33
 63 <210> SEQ ID NO: 4
 64 <211> LENGTH: 28
 65 <212> TYPE: DNA
 66 <213> ORGANISM: Artificial Sequence
 68 <220> FEATURE:
 69 <223> OTHER INFORMATION: primer
 72 <400> SEQUENCE: 4

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73 gatcctcgag tggcttgca ctgcgtct          28
76 <210> SEQ ID NO: 5
77 <211> LENGTH: 27
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: primer
85 <400> SEQUENCE: 5
86 atctctagaa tgctggcgct actgtgt          27
89 <210> SEQ ID NO: 6
90 <211> LENGTH: 34
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: primer
98 <400> SEQUENCE: 6
99 atcgaatcct caggcggcct tgcactcgct ctct          34
102 <210> SEQ ID NO: 7
103 <211> LENGTH: 30
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: primer
111 <400> SEQUENCE: 7
112 gatcctcgag tggacggcg aggactcggc          30
115 <210> SEQ ID NO: 8
116 <211> LENGTH: 31
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: primer
124 <400> SEQUENCE: 8
125 gatcctcgag tcaggcggcc ttgcactcgc t          31
128 <210> SEQ ID NO: 9
129 <211> LENGTH: 30
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: primer
137 <400> SEQUENCE: 9
138 gatcctcgag tggacggcg aggactcggc          30
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142 <211> LENGTH: 31
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: primer
150 <400> SEQUENCE: 10
151 aatgctcgag tcactctgag tgctcccgcg c          31

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154 <210> SEQ ID NO: 11
155 <211> LENGTH: 240
156 <212> TYPE: PRT
157 <213> ORGANISM: Homo sapiens
159 <220> FEATURE:
160 <221> NAME/KEY: PEPTIDE
161 <222> LOCATION: (1)..(240)
162 <223> OTHER INFORMATION: Human EC SOD
165 <400> SEQUENCE: 11
166 Met Leu Ala Leu Leu Cys Ser Cys Leu Leu Ala Ala Gly Ala Ser
167 1 5 10 15
169 Asp 'Ala Trp Thr Gly Glu Asp Ser Ala Glu Pro Asn Ser Asp Ser Ala
170 20 25 30
172 Glu Trp Ile Arg Asp Met Tyr Ala Lys Val Thr Glu Ile Trp Gln Glu
173 35 40 45
175 Val Met Gln Arg Arg Asp Asp Asp Gly Thr Leu His Ala Ala Cys Gln
176 50 55 60
178 Val Gln Pro Ser Ala Thr Leu Asp Ala Ala Gln Pro Arg Val Thr Gly
179 65 70 75 80
181 Val Val Leu Phe Arg Gln Leu Ala Pro Arg Ala Lys Leu Asp Ala Phe
182 85 90 95
184 Phe Ala Leu Glu Gly Phe Pro Thr Glu Pro Asn Ser Ser Arg Ala
185 100 105 110
187 Ile His Val His Gln Phe Gly Asp Leu Ser Gln Gly Cys Glu Ser Thr
188 115 120 125
190 Gly Pro His Tyr Asn Pro Leu Ala Val Pro His Pro Gln His Pro Gly
191 130 135 140
193 Asp Phe Gly Asn Phe Ala Val Arg Asp Gly Ser Leu Trp Arg Tyr Arg
194 145 150 155 160
196 Ala Gly Leu Ala Ala Ser Leu Ala Gly Pro His Ser Ile Val Gly Arg
197 165 170 175
199 Ala Val Val Val His Ala Gly Glu Asp Asp Leu Gly Arg Gly Gly Asn
200 180 185 190
202 Gln Ala Ser Val Glu Asn Gly Asn Ala Gly Arg Arg Leu Ala Cys Cys
203 195 200 205
205 Val Val Gly Val Cys Gly Pro Gly Leu Trp Glu Arg Gln Ala Arg Glu
206 210 215 220
208 His Ser Glu Arg Lys Lys Arg Arg Arg Glu Ser Glu Cys Lys Ala Ala
209 225 230 235 240
212 <210> SEQ ID NO: 12
213 <211> LENGTH: 231
214 <212> TYPE: PRT
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: TAT-EC SOD fusion protein
221 <400> SEQUENCE: 12
222 Arg Lys Lys Arg Arg Gln Arg Arg Arg Trp Thr Gly Glu Asp Ser Ala
223 1 5 10 15
225 Glu Pro Asn Ser Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys

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226 20 25 30
228 Val Thr Glu Ile Trp Gln Glu Val Met Gln Arg Arg Asp Asp Asp Gly
229 35 40 45
231 Thr Leu His Ala Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala
232 50 55 60
234 Ala Gln Pro Arg Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro
235 65 70 75 80
237 Arg Ala Lys Leu Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu
238 85 90 95
240 Pro Asn Ser Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu
241 100 105 110
243 Ser Gln Gly Cys Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val
244 115 120 125
246 Pro His Pro Gln His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp
247 130 135 140
249 Gly Ser Leu Trp Arg Tyr Arg Ala Gly Leu Ala Ala Ser Leu Ala Gly
250 145 150 155 160
252 Pro His Ser Ile Val Gly Arg Ala Val Val Val His Ala Gly Glu Asp
253 165 170 175
255 Asp Leu Gly Arg Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala
256 180 185 190
258 Gly Arg Arg Leu Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu
259 195 200 205
261 Trp Glu Arg Gln Ala Arg Glu His Ser Glu Arg Lys Lys Arg Arg Arg
262 210 215 220
264 Glu Ser Glu Cys Lys Ala Ala
265 225 230
268 <210> SEQ ID NO: 13
269 <211> LENGTH: 218
270 <212> TYPE: PRT
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: TAT-delta HD/EC SOD fusion protein
277 <400> SEQUENCE: 13
278 Arg Lys Lys Arg Arg Gln Arg Arg Arg Trp Thr Gly Glu Asp Ser Ala
279 1 5 10 15
281 Glu Pro Asn Ser Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys
282 20 25 30
284 Val Thr Glu Ile Trp Gln Glu Val Met Gln Arg Arg Asp Asp Asp Gly
285 35 40 45
287 Thr Leu His Ala Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala
288 50 55 60
290 Ala Gln Pro Arg Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro
291 65 70 75 80
293 Arg Ala Lys Leu Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu
294 85 90 95
296 Pro Asn Ser Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu
297 100 105 110
299 Ser Gln Gly Cys Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val

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300 115 120 125
 302 Pro His Pro Gln His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp
 303 130 135 140
 305 Gly Ser Leu Trp Arg Tyr Arg Ala Gly Leu Ala Ala Ser Leu Ala Gly
 306 145 150 155 160
 308 Pro His Ser Ile Val Gly Arg Ala Val Val Val His Ala Gly Glu Asp
 309 165 170 175
 311 Asp Leu Gly Arg Gly Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala
 312 180 185 190
 314 Gly Arg Arg Leu Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu
 315 195 200 205
 317 Trp Glu Arg Gln Ala Arg Glu His Ser Glu
 318 210 215
 321 <210> SEQ ID NO: 14
 322 <211> LENGTH: 231
 323 <212> TYPE: PRT
 324 <213> ORGANISM: Artificial Sequence
 326 <220> FEATURE:
 327 <223> OTHER INFORMATION: R9-EC SOD fusion protein
 330 <400> SEQUENCE: 14
 331 Arg Arg Arg Arg Arg Arg Arg Arg Trp Thr Gly Glu Asp Ser Ala
 332 1 5 10 15
 334 Glu Pro Asn Ser Asp Ser Ala Glu Trp Ile Arg Asp Met Tyr Ala Lys
 335 20 25 30
 337 Val Thr Glu Ile Trp Gln Glu Val Met Gln Arg Arg Asp Asp Asp Gly
 338 35 40 45
 340 Thr Leu His Ala Ala Cys Gln Val Gln Pro Ser Ala Thr Leu Asp Ala
 341 50 55 60
 343 Ala Gln Pro Arg Val Thr Gly Val Val Leu Phe Arg Gln Leu Ala Pro
 344 65 70 75 80
 346 Arg Ala Lys Leu Asp Ala Phe Phe Ala Leu Glu Gly Phe Pro Thr Glu
 347 85 90 95
 349 Pro Asn Ser Ser Arg Ala Ile His Val His Gln Phe Gly Asp Leu
 350 100 105 110
 352 Ser Gln Gly Cys Glu Ser Thr Gly Pro His Tyr Asn Pro Leu Ala Val
 353 115 120 125
 355 Pro His Pro Gln His Pro Gly Asp Phe Gly Asn Phe Ala Val Arg Asp
 356 130 135 140
 358 Gly Ser Leu Trp Arg Tyr Arg Ala Gly Leu Ala Ser Leu Ala Gly
 359 145 150 155 160
 361 Pro His Ser Ile Val Gly Arg Ala Val Val Val His Ala Gly Glu Asp
 362 165 170 175
 364 Asp Leu Gly Arg Gly Gly Asn Gln Ala Ser Val Glu Asn Gly Asn Ala
 365 180 185 190
 367 Gly Arg Arg Leu Ala Cys Cys Val Val Gly Val Cys Gly Pro Gly Leu
 368 195 200 205
 370 Trp Glu Arg Gln Ala Arg Glu His Ser Glu Arg Lys Lys Arg Arg Arg
 371 210 215 220
 373 Glu Ser Glu Cys Lys Ala Ala

VERIFICATION SUMMARY

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